

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/789,273
Source: IF100
Date Processed by STIC: 07/26/2005

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 07/26/2005

PATENT APPLICATION: US/10/789,273

TIME: 09:35:37

Input Set : N:\Crf3\RULE60\10789273.raw

Output Set: N:\CRF4\07262005\J789273.raw

```

1 <110> APPLICANT: Basi, Guriq
2   Saldanha, Jose
3   Yednock, Ted
4 <120> TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
5   BETA-AMYLOID PEPTIDE
6 <130> FILE REFERENCE: ELN-002CP
7 <140> CURRENT APPLICATION NUMBER: US/10/789,273
8 <141> CURRENT FILING DATE: 2004-02-27
9 <150> PRIOR APPLICATION NUMBER: US/10/388,389
10 <151> PRIOR FILING DATE: 2003-03-12
11 <150> PRIOR APPLICATION NUMBER: US 10/010,942
12 <151> PRIOR FILING DATE: 2001-12-06
13 <150> PRIOR APPLICATION NUMBER: US 60/251,892
14 <151> PRIOR FILING DATE: 2000-12-06
15 <160> NUMBER OF SEQ ID NOS: 63
16 <170> SOFTWARE: FastSEQ for Windows Version 4.0
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 396
20 <212> TYPE: DNA
21 <213> ORGANISM: Mus musculus
22 <220> FEATURE:
23 <221> NAME/KEY: CDS
24 <222> LOCATION: (1)...(396)
25 <220> FEATURE:
26 <221> NAME/KEY: sig_peptide
27 <222> LOCATION: (1)...(60)
28 <400> SEQUENCE: 1
29   atg atg agt cct gcc cag ttc ctg ttt ctg tta gtg ctc tgg att cgg      48
30   Met Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg
31   -20                               -15                               -10                               -5
32   gaa acc aac ggt tat gtt gtg atg acc cag act cca ctc act ttg tcg      96
33   Glu Thr Asn Gly Tyr Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser
34   1                               5                               10
35   gtt acc att gga caa cca gcc tcc atc tct tgc aag tca agt cag agc     144
36   Val Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser
37   15                               20                               25
38   ctc tta gat agt gat gga aag aca tat ttg aat tgg ttg tta cag agg     192
39   Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg
40   30                               35                               40
41   cca ggc cag tct cca aag cgc cta atc tat ctg gtg tct aaa ctg gac     240
42   Pro Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp
43   45                               50                               55                               60
44   tct gga gtc cct gac agg ttc act ggc agt gga tca ggg aca gat ttt     288

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45      Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe
46                      65                      70                      75
47      aca ctg aaa atc agc aga ata gag gct gag gat ttg gga ctt tat tat      336
48      Thr Leu Lys Ile Ser Arg Ile Glu Ala Glu Asp Leu Gly Leu Tyr Tyr
49                      80                      85                      90
50      tgc tgg caa ggt aca cat ttt cct cgg acg ttc ggt gga ggc acc aag      384
51      Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gly Gly Thr Lys
52                      95                      100                      105
53      ctg gaa atc aaa                                          396
54      Leu Glu Ile Lys
55      110
57 <210> SEQ ID NO: 2
58 <211> LENGTH: 132
59 <212> TYPE: PRT
60 <213> ORGANISM: Mus musculus
61 <220> FEATURE:
62 <221> NAME/KEY: SIGNAL
63 <222> LOCATION: (1)...(20)
64 <400> SEQUENCE: 2
65      Met Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg
66      -20                      -15                      -10                      -5
67      Glu Thr Asn Gly Tyr Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser
68                      1                      5                      10
69      Val Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser
70                      15                      20                      25
71      Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg
72                      30                      35                      40
73      Pro Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp
74      45                      50                      55                      60
75      Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe
76                      65                      70                      75
77      Thr Leu Lys Ile Ser Arg Ile Glu Ala Glu Asp Leu Gly Leu Tyr Tyr
78                      80                      85                      90
79      Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gly Gly Thr Lys
80                      95                      100                      105
81      Leu Glu Ile Lys
82      110
84 <210> SEQ ID NO: 3
85 <211> LENGTH: 414
86 <212> TYPE: DNA
87 <213> ORGANISM: Mus musculus
88 <220> FEATURE:
89 <221> NAME/KEY: CDS
90 <222> LOCATION: (1)...(414)
91 <220> FEATURE:
92 <221> NAME/KEY: sig_peptide
93 <222> LOCATION: (1)...(57)
94 <400> SEQUENCE: 3
95      atg aac ttc ggg ctc agc ttg att ttc ctt gtc ctt gtt tta aaa ggt      48

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96      Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly
97              -15              -10              -5
98      gtc cag tgt gaa gtg aag ctg gtg gag tct ggg gga ggc tta gtg aag      96
99      Val Gln Cys Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys
100              1              5              10
101      cct gga gcg tct ctg aaa ctc tcc tgt gca gcc tct gga ttc act ttc      144
102      Pro Gly Ala Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
103              15              20              25
104      agt aac tat ggc atg tct tgg gtt cgc cag aat tca gac aag agg ctg      192
105      Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Asn Ser Asp Lys Arg Leu
106              30              35              40              45
107      gag tgg gtt gca tcc att agg agt ggt ggt ggt aga acc tac tat tca      240
108      Glu Trp Val Ala Ser Ile Arg Ser Gly Gly Gly Arg Thr Tyr Tyr Ser
109              50              55              60
110      gac aat gta aag ggc cga ttc acc atc tcc aga gag aat gcc aag aac      288
111      Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn
112              65              70              75
113      acc ctg tac ctg caa atg agt agt ctg aag tct gag gac acg gcc ttg      336
114      Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Leu
115              80              85              90
116      tat tat tgt gtc aga tat gat cac tat agt ggt agc tcc gac tac tgg      384
117      Tyr Tyr Cys Val Arg Tyr Asp His Tyr Ser Gly Ser Ser Asp Tyr Trp
118              95              100              105
119      ggc cag ggc acc act gtc aca gtc tcc tca      414
120      Gly Gln Gly Thr Thr Val Thr Val Ser Ser
121      110              115
123 <210> SEQ ID NO: 4
124 <211> LENGTH: 138
125 <212> TYPE: PRT
126 <213> ORGANISM: Mus musculus
127 <220> FEATURE:
128 <221> NAME/KEY: SIGNAL
129 <222> LOCATION: (1)...(19)
130 <400> SEQUENCE: 4
131      Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly
132              -15              -10              -5
133      Val Gln Cys Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys
134              1              5              10
135      Pro Gly Ala Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
136              15              20              25
137      Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Asn Ser Asp Lys Arg Leu
138              30              35              40              45
139      Glu Trp Val Ala Ser Ile Arg Ser Gly Gly Gly Arg Thr Tyr Tyr Ser
140              50              55              60
141      Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn
142              65              70              75
143      Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Leu
144              80              85              90
145      Tyr Tyr Cys Val Arg Tyr Asp His Tyr Ser Gly Ser Ser Asp Tyr Trp

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146          95          100          105
147      Gly Gln Gly Thr Thr Val Thr Val Ser Ser
148      110          115
150 <210> SEQ ID NO: 5
151 <211> LENGTH: 132
152 <212> TYPE: PRT
153 <213> ORGANISM: Artificial Sequence
154 <220> FEATURE:
155 <221> NAME/KEY: SIGNAL
156 <222> LOCATION: (1)...(20)
157 <223> OTHER INFORMATION: humanized 3D6 light chain variable region
158 <400> SEQUENCE: 5
159      Met Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg
160      -20          -15          -10          -5
161      Glu Thr Asn Gly Tyr Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro
162          1          5          10
163      Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser
164          15          20          25
165      Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Lys
166          30          35          40
167      Pro Gly Gln Ser Pro Gln Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp
168      45          50          55          60
169      Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
170          65          70          75
171      Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
172          80          85          90
173      Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gln Gly Thr Lys
174          95          100          105
175      Val Glu Ile Lys
176      110
178 <210> SEQ ID NO: 6
179 <211> LENGTH: 125
180 <212> TYPE: PRT
181 <213> ORGANISM: Homo sapiens
182 <220> FEATURE:
183 <221> NAME/KEY: SIGNAL
184 <222> LOCATION: (1)...(13)
185 <400> SEQUENCE: 6
186      Met Gly Leu Leu Met Leu Trp Val Ser Gly Ser Ser Gly Asp Ile Val
187          -10          -5          1
188      Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro Ala
189          5          10          15
190      Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr
191      20          25          30          35
192      Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu
193          40          45          50
194      Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe
195          55          60          65
196      Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val

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197          70          75          80
198      Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala Leu Gln Thr
199          85          90          95
200      Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
201      100          105          110
203 <210> SEQ ID NO: 7
204 <211> LENGTH: 100
205 <212> TYPE: PRT
206 <213> ORGANISM: Homo sapiens
207 <400> SEQUENCE: 7
208      Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
209          1          5          10          15
210      Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
211          20          25          30
212      Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
213          35          40          45
214      Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
215          50          55          60
216      Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
217          65          70          75          80
218      Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
219          85          90          95
220      Leu Gln Thr Pro
221          100
223 <210> SEQ ID NO: 8
224 <211> LENGTH: 138
225 <212> TYPE: PRT
226 <213> ORGANISM: Artificial Sequence
227 <220> FEATURE:
228 <223> OTHER INFORMATION: Humanized 3D6 heavy chain variable region
229 <220> FEATURE:
230 <221> NAME/KEY: SIGNAL
231 <222> LOCATION: (1)...(19)
232 <400> SEQUENCE: 8
233      Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly
234          -15          -10          -5
235      Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
236          1          5          10
237      Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
238          15          20          25
239      Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
240          30          35          40          45
241      Glu Trp Val Ala Ser Ile Arg Ser Gly Gly Gly Arg Thr Tyr Tyr Ser
242          50          55          60
243      Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
244          65          70          75
245      Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu
246          80          85          90
247      Tyr Tyr Cys Val Arg Tyr Asp His Tyr Ser Gly Ser Ser Asp Tyr Trp

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VERIFICATION SUMMARY

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